Appln. No.: 10/563,194

Page 2

Amendments to the Specification:

Please replace the first paragraph after the title (lines 3-5) with the following

paragraph:

This application is the National Stage application of PCT/DK2004/000478 filed on

July 2, 2004, which claims benefit to Danish Application No. PA 2003 01010 filed on July 3,

2003 and U.S. provisional Application No. 60/484,923, filed July 3, 2003 (now expired),

which application(s) are incorporated herein by reference.

Please replace the third paragraph on page 17, lines 20-24, with the following

paragraph:

Pfam consensus: a consensus sequence derived from a large collection of protein

multiple sequence alignments and profile hidden Markov models used to identify conserved

protein domains (Bateman et al., 2002, Nucleic Acids Res. 30: 276-80; and searchable on

http://www. the internet at sanger.ac.uk/Software/Pfam/ and on NCBI at http://www.

ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi.

Please replace the fourth paragraph on page 17, lines 26-30, with the following

paragraph:

Protein domain prediction: sequences are analyzed by BLAST (www.

(ncbi.nlm.nih.gov/BLAST/) and PredictProtein (www.

(emblheidelberg.de/predictprotein/predictprotein). Signal peptides are predicted by

SignalP v. 1.1 (www. (cbs.dtu.dk/services/signalP/) and transmembrane regions are

predicted by TMHMM v. 2.0 (www. (cbs.dtu.dk/services/TMHMM/).

Please replace the paragraph on page 19, lines 19-31 through page 20, lines 1-4, with

the following paragraph:

fb.us.4029424.01

Appln. No.: 10/563,194

Page 3

Substantially identical: refers to two nucleic acid or polypeptide sequences that have at least about 60%, preferably about 65%, more preferably about 70%, further more preferably about 80%, most preferably about 90 or about 95% nucleotide or amino acid residue identity when aligned for maximum correspondence over a comparison window as measured using one of the sequence comparison algorithms given herein, or by manual alignment and visual inspection. This definition also refers to the complement of the test sequence with respect to its substantial identity to a reference sequence. A comparison window refers to any one of the number of contiguous positions in a sequence (being anything from between about 20 to about 600, most commonly about 100 to about 150) which may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Optimal alignment can be achieved using computerized implementations of alignment algorithms (e.g., GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis. USA) or BLAST analyses available on the site: (www.nebi.nlm.nih.gov/) (ncbi.nlm.nih.gov/)

Please replace the paragraph on page 53, lines 5-21, with the following:

The NFR5 Nod-factor binding proteins encoded by the *NFR5* alleles of *Lotus japonicus* ecotype GIFU (gene sequence: SEQ ID No: 7; protein sequence: SEQ ID No: 24 & 25), and *Lotus filicaulis* (gene sequence SEQ ID No: 30; protein sequence SEQ ID No: 31) have been compared, and found to show diversity in their primary structure. Using the sequence information available for the *Lotus NFR5* gene together with the pea SYM10 gene (Table 12), the alleles from different ecotypes or varieties of *Lotus*, pea and other legumes can now be identified, and used directly in breeding programs. By further way of example, the nucleic acid sequence of the *Phaseolus vulgaris NFR5* gene (SEQ ID No: 39) has facilitated the identification of a molecular marker for two different *NFR5* alleles in the *Phaseolus vulgaris* lines Bat93 and Jalo EEP558, that is based on a single nucleotide difference creating an Apol restriction site (RAATTY) in line Bat93, wherein R stands for A or G, Y for C or T. A partial sequence of the *NFR5* gene comprising the Apol site molecular marker identified in line Bat93 is shown in bold type:

Appln. No.: 10/563,194

Page 4

CACAGGACATATTGAGTGAAAACAACTATGGTCA**AAATTT**CACTGCCGC AAGCAACCTTCCAGTTTTGATCCCAGTTACA(SEQ ID No: 55)

Please replace the paragraph on page 53, lines 22-25, with the following:

The absence of this Apol site in the comparable *NFR5* partial sequence of line Jalo EEP558 is shown in bold type:

CACAGGACATATTGAGTGAAAACAACTATGGTCA**AAACTT**CACTGCCGC AAGCAACCTTCCAGTTTTGATCCCAGTTACA<u>(SEQ ID No: 56)</u>

Please replace Table 1 on page 55 with the following:

Table 1 Alignment of Lotus, Glycine and Phaseolus NFR5 protein sequences

			32				
		HAVEF	3	3	an e e e e e e e e e e e e e e e e e e e	\$6	
Cotua	3	PLAYPY	SECTIONS	LLCTHIANES	EX18GADLEC.	PYCISOPSCRY REGSOPSCRY PORESOPSCRY	26
Glycine	3	MARKET PRODUCT	RECORD STATE	Presentance.	CCOMMANNEC.	ARDRODUCES	55
Phaseolus	2	KRYFFVELTL .	SACCELYVYLM:	ಕ್ಷಕ್ಷರ್ಷ 🦠 🦠	COMMITTERS	Peneedecky,	86
			-3	- 6	9	202	
Section	\$	SYTYTAGERN	LLSUISTED :	FUSSPLEIA	ASSTDACEDE?	PAROCALTAR S	500
Giyeine	3	SYTYIAGERK	FLELTMENS.	FOTSPLEIAR	ASSESSMENT .	SWKDOWLLUP .	500
Phasepius	35	SALA 13000500	PLSE/282288	SUPSPLETAR	ASSECUENCES	PTP-GOATTY TAKTOATTAN TARGOATTAN	100
7.111.		A1994 A118 44 A118 A118	enedeciation includes the	- public deserges as research	104400 children con con 10004	grand activities and a	444
		3.3	12	13	18	350	
Letus	10	327/72/78/08/08/08	SAMPLE VOLVES	See Assessment	5 NORSKY 2000000 1	MANUS DESIGNATION IS	150
Glyciss	1.0	1000,000,000,000,000	100 100 100 100 100 100 100 100 100 100	MINISTER FRANCE	CONTRACTOR AND	ygasepoves Vydlaifylse	
Fhacenius	10	A STATE STANKES	Lunio Eruc	Opportunition (TAZMPIAMOS.	4500 KON A 400 E	386
34:000 6002 002	14	A 1 Print Translet Co.	LHC15(PTMA)	MARKET SHIP	Programma single .	Assiria Name &	726
		3.3		3-8			
Y + 4	2 a or	1.6 Territoria		18	19	260	an exist
	1.3	(recessors)	Excersor 22K	warmani care	A S. C. ASAR FRANCIA (VOCABARAGA	266
Glywiss	1.5	SKLFIGICAA	EDTECTORS.	MODERATE AND	CLANSACTOR .	velveryeg velveryeg ververeg	266
Fharestus	15	sareraton"	I DERCECES R	MOCONGLESS.	SURVANCE BUDGES	ARMARKETCH .	200
		31		23	24	253	
Sorus	3.0	S.FADI LITENR	YCKECTERIN	FELFESAMO :	PELOCHSERG	XXXXXXBGGV	255
diyeine	29	ANN MET DAG 2	YCCOMPTABLES	LOULINGTA	POLICEPSIO PATYNSISSO PRIOCHASES PATYNSISSO	RACHERREVI	250
Finesociae	3.9	SPCDITURNS.	YGMPTAANN	Cantranac	PULICEPSDU.	SWELDER HORSE	250
		Andreas and appropriate of	Section of Section 21 - 24.	61.0040000000000000000000000000000000000	ANT OUR MANNE STORY	other and an arrange	
		28	27	28	28	380	
ಹಿಲಕಬಕ	3.3	14055345577	TRUE TOWN	พ.ศ. 2 สามารถสมาชาวารถ (การณา	STARRAGES OF	RYY, COUGANON	500
Wiyedne	38	100000000000000000000000000000000000000	X21.X22.X.122.2.X24	NOVEY AND AND AND A	Ses erapron	NAT A STORE OF THE	320
Phasentus	28			***********	on or or or or or or	KILLOTVSCTY KILLOTVSCTY KILLOTVSCTY	
6.00.66037788	8.3	SHOSHOCT PO	KARBURE	Acres as a reference	POADSMEZAL	2444534263XX	>##
		20.	33	33		يتمند	
Latus	30	damenta ina	32 Secretario	o section of the section of	34	350	42.00
		DISCOURT AND ASSOCIA	A LOOP A KAND WAS	NAC 34 KO 4 S S S S	9663 COS VENT	DOLDERAMINE!	350
Біроіне	3.9	arrorerum.	imminute.	Warnesania .	ASTEGRIVAY ASTEGRICAY ASTEGRICAY	swaarn Add	788
Phasecius	38	SECTION REPORTS	2 recommende	SOME SERVICE	We ledge Army	SOCKSHOP (ALRE)	350
		44.	1.00		2.5 4		
1.			37	38	29	488	
Leetus	3.8	RESTRICTION	CHLVRIATION	2010C0C174	YEYAENGSLA YEYAENGSLA	2014/2012	900
Stil protinse	3.8	ECKITACKANH!	CHEVELECTER	SCHOOLS	CIPERRAFE	BWLFSKSC80	600
Phascolus	3.5	SUNTINGUIH	CHENKI WILKS	SCHOOL SAN	YETAKWOSUK	Bellenksche	400
		41	4.2	63	44	458	
locus	60	ROTENSLING	CALLETECS.	AVSLOYNER	TYPETTHEN	Tresitades.	450
Gigarine	40	FERENASE, TW	C26 (3840) (0)	ANCIONNER!	ACCRIVATION	1883314D58	450
Phaseclas	40	STIPHSLYW TRUSSLELTW TRUSSLELTW	CORTELLANDA	SHELCYNISHS	ATTRIVEREDI N	TEENILLDES	450
		Transferrage Sections				. procedura and appropriate (1990)	
		46	49	49	49 LIELTORKA	560	
Lorus	45	PRAKTANDAM	A SOUTH POPONION	XTDVPANSVX	LC SELETWRKA	MITKENSBVV	800
G3yesne	4.5	PROUGHANNEN.	A STOTE THE PROPERTY.	SCHOOL PROSTOR	1.7255,7909984	SOTTO CONTRACTOR	500
Phoneolus	65	Peartanpem Peartanpem	A SOUTH THE OWNER	ac v recreits seconds	1.2 erc (1990a) x - 1	CONTRACTOR OF THE STATE OF THE	960
- Therefore Web	* -	Automobile Marketing	PHOLICAL STREET	State	were and a supply of	SW 930803505 U.S.	300
		×8.	8.9	53	20.4	ena	
LOVER	8.0	MEMSCHARTE MEMSCHARTE MEMSCHARTE	5.00000000	topologica de la companya del companya del companya de la companya	2001 2003 20	332	000
	200		STATE OF THE PARTY OF	reconstruction and			980
Glycine Phaseolus	50	Minutes and the second	CONTRACTOR OF THE PARTY OF THE	24400 C S C C C C C C C C C C C C C C C C C	2.2 E (1.15 Septembre 2	ASIACON LAG	888
supposecrate.	50	301420346003	HANGE STREET, ST.	KKSMI KETTER	(GARIOLATER)	ASEAWNCTAE)	\$50
						1000	
Marine and the second		36	onverse on a	25	39 300000000000000000000000000000000000	689 	4.4
Lotus	55	KSLSRPSMAS KSLSRPSLAB	TALEST TARE	QESNETTERS)	#42820190AMD	CANTALET !	600
Ciyaine	5.5	K\$132271AB	avisisier :	PEP-ATLERS	C42 82122 222	1000	600
Massolus	88	KSI&PPTIAE	Augustur :	BEE-VITTERS	1T9SCLDYEA		600
		£1.	62	63.	કલ	680	Abb feetah in 197
Lotus	6.3	≸	13.79	1919		Sugar.	688 SEQ ID NO: 8
Tîyeine	2.5	3	2	·		× 4 4 4	#50 <u>SEQ</u> ID NO: 48
Phasecles	£ 2	Ř	****	11,00	1888	***	650 <u>SBO ID NO: 40</u>

Please replace Table 3 on page 57 with the following:

Table 3

Align					sequençe		
Fision	1	WKTREGFFE.	9 - 3 ()	MARRIED LANGE	dialacytyn Clalacytyn Clalacytyn	F	50
Fisur	1	NORTH SACRET FOL.	35.400	KAMESOLAKEC	ELLLAETTV#		80
Lexus	į.	MKLKTGLLLF	elfrichense.	MARSHCPROC:	CLALAGETT	Povettont :	\$0
~ 2	.2		3	S	<u> </u>	CECTORANO CECTORANO TRE	12.44.1
P (ဆုမှုက	S S	A.B. 200 200 200 200 200 200 200 200 200 20	ELIKIANANA	SAARSHUMEN.	XXXXXXXXXXXX	0.000,000,000,000	\$66
Pisus	. 3	20.000.000.000.000	generalise.	areanimmert.	2322818282	08031989888	\$66
Rayus	Ş	TENGES I VES	M403 3 28 8 9 8	sista restratifi	permarker!	COCTOGRAM	100
Swiften S	- 24	13	12 1	13	314 314 (82 94 (37)	190 Trykasymyr	4 L S.L.N
Pingum Comment	16 16	HALBELLINGS	CZE X CA CE SOME A C	KANTANAMA	ANTENDER DESCRIPTION	Thekwasomen	190
Fisum Letus	10	CONTRACTOR MANAGE	500 4 0/2/2 30000 C	KARDER ARROW	XXPNEYDPSH	Transcanal	196
7857159:		SERVE STRONGSON.	detter seine 2	innerskinder	Washinston to	The ANNEXANCE	158
		16	SAME TO LANGE	1.6	19	vigarellare	Car.
Pi sum	3.5	ANCORPORATE 2	BROTHSON ST	PICK PROTECTION.	TANKONCOROS	A160 1889 489	200
Pisus	3.5	400000000000000000000000000000000000000	AND THE STATE	Panachanak.	THREE CINCOLOGY	Cicerbara Cicerbara	200
LOURS	1.9	instruction Sa	9mme21710	ka stanna ham	Contrate Contrate.	C1004BS8.40	200
Fix ann	*.*	32	22	23	34	250	***
PS stan	20	PSKCSSVVFF	Manakesety	PERPER GLG	WGAAAG181	GIPAGGAN Y	390
Fisum	20	1.2 8 (52221 8.3)	2/3V/SV/BRBBB	427 (42. E. GAC)	323.910131.	GYPAYELEY GYPYLLLLA	390
Lotus	28	PERCENTAR:	NUMBER AND ASTRACT	TTENKERGUR	262040031231	PATE SERVICE	252
and the second		36	27	128	29	196 Gorchoda Gorchoda	
Pi sur	25	CITIXYFOX	RESERVED OF	ARTALISMON	ANGEGEVEY:	acammares .	300
Pisses	33	CLIVEYFORK	BBBR1112	VEXALETICO	MASSESSEE	20220000000000	800
Locus	3.5	(243.ASA) ORK	RESEARLETO	\$ districtions	- MANAGE MESTERS 1	SCSSCPOTAS	300
	v. v.	33	3.3	AA A STUDENS SEEDER A	34	350	. 1. 1. 1.
Fishion Mission	28	JAGGEROIRVA .	NATES BY THE CO	wowarmen or	nkiojošeca nkiojošeca	A3.24.A1.00.024.	350
Fisum Lotus	38 38	WOOD COLUMN	MATERIAL SECTION	MANAGEMENT OF THE	DATE OF STREET	OFFICE PROPERTY.	150
. accessors	.29	Washington,	seasonanies.	\$550 STORY STATES	nniopoerga)	VI IMBURGES.	-3:00W.
P.i. conto	38	36 900 3664030	37 3800000000000000000000000000000000000	38	29	\$00 TTTTTTTTTTT	400
Picas	39	that you and only the o	Superior Control	Koonsonser ser on	REIGYCVEGS REIGYCVEGS	A DATAMERICA CO.	400
\$000	35	3/4 / 6/6/30/20/20	STSP3.CELEV	5 712 712 12 12 12 12 12 12 12 12 12 12 12 12 1	MF1GACABGB	A PAINARRIAN	300
2000	. 0.0	100000000000000000000000000000000000000		SECTION STATES	- ARMANA ARRAM	meen Newsons o	***
Julia:		M	本意 (2000) - 2017-2018-2018	43	34	450	
#18000	48	Derlogeleit Gerlogeleit	DKRELEWSER	WULNIANSARS:	TELINESIZAB	WIIHRIWKSA.	950
F18000	45 40	SHIP NOT NOT	10K8 F0 F98003 8	WILKLUSARG	LEYIHSHTVP LEYIHSHTVP LEYIHSHTVP LEYIHSHTVP	WILHKUYESA:	450
Locus	**	OKTOOKTHOE	PRESERVED AND A STATE OF THE PARTY OF THE PA	an estronomo:	9983 1086 135	ATMENTAGE	455
War and the Control		artement fi	- 47 - 1115 Silver 1905 19	48	49	596	. www.co
Finan	*5	MESSERMAN	NYADIOGLIFEL.	Listenson Tierr	RLVGTFGTHF RLVGTFGTHR	SELWLANDAR	563
Pisus Lotus	* \$ \$	MANADENIA	AVMORPHIA NO	TRANSMETTERS :	RLVCTTCYNR BLACTTGYNP	PETALITUDES :	568 568
SARAGE.	*2	demonstration of	Section Services	98000000000000000000000000000000000000	Service Secretary	Section and a	560
let in m	97.70	Si Suremane sous (53	52	54	922	888
Fisus Fisus	50 55	Sections of the Control of the Contr	VIJABLISAR :	MEDINICESAN	PERFECTIVALS ABSKULVALS	MARINET SEC	550
ADEUS	88	September 2000 Car	ACCOUNT NAME	MANAGES .	amount circ a	enectable pass	550 550
8075.010	22	Separation and the second	Sec. antenness.	- Marie Carrier Sa	**************************************	and and an area.	224
Di some		92 Caccompanae	57	58	TRUMPLLERS)	500	anis.
Alama Piamo	\$\$ \$\$	SOLIKALIOUSS :	CONTRACTOR CONTRACTOR	CANADA CARACTER CO.	TRINGILLAGE	March Colonic New A	663 663
EU BOOK EGERTE	25	ENTERPREDE	TOTAL P. 1709 6	ENTROPHOLES	TRINPLLERS	MINIST STUDY CAND	600
XID-CAD		- Charlette Hall	**************************************	HE CHARLES	41400000000000000000000000000000000000	Chroma succession	pwy.
Pisus	85	St. Worker St.	62 37 0988(2 17	63	£4	850	450 COA TR MA - 50
8'3 8'30'	80 60	LESPFEDCOD	OTSTERQUE.	TOT T CATE		100 cg.	650 <u>SĐQ ID NO: 52</u> 680SĐQ ID NO: 54
aram Later	80 80	TOOFFEECUD.	2883890077				480 SEQ ID NO: 24
60000	25.00	SHEET HARRISH	~ ad emanifold.	11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			*** <u>AES ED NO: 24</u>

Please replace Table 11 on page 64 with the following:

TABLE 11

]	Molecular m	arkers for NFR5 allele breeding in Lotus	
Marker	Genetic	Lotus	Microsatellite sequence	SEQ ID NO:
	distance from	Ecotype		
	NFR5 locus			
TM0272	2.9 cM	MG-20	18xCT	
		Gifu	12xCT	
TM0257	1.0 cM	MG-20	10xAAG	
		Gifu	7xAAG	
LjT13i23Sfi		Gifu	TTTTGCTGCAGCAAGTCAGACTGTTAGAGGA	57
		Fili	TTTTGCTGCAACAAGTC G GACTGTTAGAGGA	58
TM0522	0 cM	MG-20	24xAT	
		Gifu	14xAT	
NFR5				
E32M54-12F	0.5 cM	MG-20	TTGGAAGTTCTTTTTA TTA GGTTAATTTTA	59
		Fili	TTGGAAGTTCTTTTTA GGTTAATTTTA	60
LJt01C03 Not	0.7 cM	Fili	CATTCCAGAAGAAAATAAGATATAATTATG	61
		MG-20	CATTCCAGAAGAAAATAAGATATAATTATG	61
		Gifu	CATTCCAGAAG - AAATAAGATATAATTATG	62
TM0168	2.2 cM	MG-20	19xAT	
		Gifu	15xAT	
TM0021	3.8 cM	MG-20	16xCT	
		Gifu	13xCT	

Please replace Table 12 on page 65 with the following:

Table 12 Nucleotide sequence variation between the pea SYM10 alleles of pea cultivars Frisson and Finale*

Frisson	Condition & decidate	TTCACAATTT	CREACAROR	GCTATETTET	declesia declesia kredechika
Finale	CTTGCATTTC	TTCACAATTT		GCTATCTTCT	
* * 1 * 1 * 1 * 1	~ * * * * * * * * * * * * * * * * * * *	* * ********	2001 1 2008 88 3 2004 88 5 5 5 60	40 50 44 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5	*****
Prisson	TAGTTCTCAT	GCCCTTTTTC	TTGCACTCAT	GITTITTGTC	ACTAATATTT
Finale	TAGTTCTCAT	GCCCTTTTC	TTGCACTCAT	GTTTTTTGTC	ACTAATATTT
	***************************************	***************************************			
Frisson				ACTITICATG	
Finale	CAGCTCAACC	ATTACAACTC	AGTGGAACAA	ACTITICATG	CCCGGTGGAT
Let 1 y 10 in the					
Frisson	TCACCTCCTT	CATGTGAAAC		TACTTTGCTC	GGTCTCCAAA
Finale	TCACCTCCTT	CAIGIGAAAC	CIAIGIGACA	TACTITGCTC	GGTCTCCAAA
Frisson	CTTTTTCAGC	ተመንቋ ልተመንቋ ልተማ	means are an arm	ATTTGATATG	A CHINA CHINENDA ED
Finale	CTTTTTGAGC			ATTTGATATG	
e a made	C T A X A A COSTOR	(2 4 158.812 4 CRUTCH	4314 (431441414	WILLIAM CONTRACTOR	FREE 1-2-4 A AREA
Frisson	CCATTGCAAA	AGCCAGTAAC	ATAGAAGATG	AGGACAAGAA	GCTGGTTGAA
Finale	CCATTGCAAA	AGCCAGTAAC	ATAGRAGATG	AGGACAAGAA	GCTGGTTGAA
					
Frisson	GGCCAAGTCT	TACTCATACC	TGTAACTTGT	GGTTGCACTA	GAAATOGOTA
Finale	GGCCAAGTCT	TACTCATACC	TGTAACTTGT	GGTTGCACTA	GAAATCGCTA
		Contract and a second contract of the contract			
Prisson	TTTCGCGAAT			AGGTGACAAC	TATTTCATAG
Finale	TTTCGCGAAT	TTCACGTACA	CAATCAAGCT	AGGTGACAAC	TATTTCATAG
Frisson	CACCAACTT	TTCATACCAG	AATCTTACAA	ATTATGTGGA	32mm333333m
Finale				ATTATGTCKSA	
a magazine	***************************************			***	A MARKA SUSTAIN NO NE NE NE NE
Frisson	TTCAACCCTA	ATCTAAGTCC	AAATCTATTG	CCACCAGAAA	TCAAAGTTGT
Finale	TTCAACCCTA	ATCTAAGTCC	AAATCTATTG	CCACCAGAAA	TCAAAGTTGT
Frisson	TGTCCCTTTA		GCCCCTCGAA		AGCAAAGGAA
Finale	TGTCCCTTTA	TTCTGCAAAT	GCCCCTCGAA	GAATCAGTTG	<u>AGCAAAGGAA</u>
Th an X in arbandi	Contract to the contract of the contract of	CONTRACTOR OF CANADANA AND			
Frisson	TAAAGCATCT			CTAATGACAA	
Finale	TAAAGCATCT	GALLACITAL	GIGIGGENGG	CTAATGACAA	1011ACCCG1
Prisson	CTARCTTCCA	AGTTTGGTGC	arcacaacro	GATATGTTTA	CONTRACTOR ASSESSMENT
Finale	GTAAGTTCCA		ATCACAAGTG	GATATGTTTA	
a manage of	S. 100 to 100 10 10 10 10 10 10 10		i i i i i i i i i i i i i i i i i i i		** * ** ** ** ** ** ** ** ** ** ** ** *
Frisson	TCAAAACTTC	ACTGCTTCAA	CCAAGGTTCC	GATTTTGATC	CCTGTGACAA
Fisale				GATTTTGATC	

Frisson				ATGGAAGAAA	
Finale	AGTTACCGGT	AATTGATCAA	CCATCTTCAA	ATGGAAGAAA	AAACAGCACT

Frisson	CAAAAACCTG CTTTTATAAT TGGTATTAGC CTAGGATGTG CTTTTTTCGT
Finale	CAAAAACCTG CTTTTATAAT TGGTATTAGC CTAGGATGTG CTTTTTTCGT
and the second second	
Frisson	TGTAGTTTTA ACACTATCAC TIGTTTATGT ATATTGTCTG AAAATGAAGA
Pinale	TGTAGTTTTA ACACTATCAC TTGTTTATGT ATATTGTCTG AAAATGAAGA
Frisson	GATTGAATAG GAGTACTTCA TTGGGGGAGA CTGCGGATAA GTTACTTTCA
Finale	GATTGAATAG GAGTACTTCA TIGGCGGAGA CTGCGGATAA GTTACTTTCA
Frisson	GGTGTTTCGG GTTATGTAAG CAAGCCAACA ATGTATGAAA TGGATGCGAT
Finale	GGTGTTTCGG GTTATGTAAG CAAGCCAACA ATGTATGAAA TGGATGCGAT
Frisson	CATGGAAGCT ACAATGAACC TEAGTGAGAA TTETAAGATT GGTGAATCG
Finale	CATGGAAGCT ACAATGAACC TGAGTGAGAA TTGTAAGATT GGTGAATC
Frisson	TTTACAAGGC TAATATAGAT GGTAGAGTTT TAGCAGTGAA AAAAATCAAG
Finale	TTTACAAGGC TAATATAGAT GGTAGAGTTT TAGCAGTGAA AAAAATCAAG
Frisson	AAAGATOCTT CTGAGGAGCT GAAAATT <mark>I</mark> TG CAGAAGGTAA ATCATGGAAA
Finale	AAAGATGCTT CTGAGGAGCT GAAAATT
0	
Frisson	TCTTGTGAAA CTTATGGGTG TGTCTTCCGA CAACGA GGA AACTGTTTCC
Finale	TCTTGTGAAA CTTATGGGTG TGTCTTCCGA CAACGAAGGA AACTGTTTCC
Frisson	TIGITIACGA GIAIGCIGAA AATGGATCAC TIGATGAGIG GITGITCICA
Finale	TIGTITACGA GTATGCTGAA AATGGATCAC TIGATGAGTG GTTGTTCTCA
	and the second of the second o
Frisson	GACTATICCA AAACTICCAA CTCGGTGGTC TCGCTTACAT GCTCTCAGAG
Finale	GAGTAGTOGA AAACTTOGAA CTOGGTGGTO TOGCTTACAT GGTCTCAGAG
Frieson	AATAACAGTA GCAGTGGATG TTGCAGTTGG TTTGCAATAC ATGCATGAAC
Pinale	ANTANCAGTA GCAGTGGATG TTGCAGTTGG TTTGCAATAC ATGCATGAAC ANTANCAGTA GCAGTGGATG TTGCAGTTGG TTTGCAATAC ATGCATGAAC
521301.0	ANIAMATIA GLAGIGATO TIGCAGIION TITOCARIRE RIGLALONG.
Frisson	ATACTTACCC AAGAATAATC CACAGAGACA TCACAAGAAG TAATATCCTT
Finale	ATACTTACCC AAGAATAATC CACAGAGACA TCACAACAAG TAATATCCTT
Frisson	CTGGATTCAA ACTITAAGGC CAAGATAGCG AATTTTTCAA TGGCCAGAAC
Finale	CTOGATTCAA ACTITAAGGC CAAGATAGCG AATTITTCAA TGGCCAGAAC
Man I area a ar	TTCAACAAAT TCCATGATGC CGAAAATCGA TGTTTTCGCT TTTGGGGTGG
Frisson Finale	TTCAACAAAT TCCATGATGC CGAAAATCGA TGTTTTCGCT TTTGGGGTGG TTCAACAAAT TCCATGATGC CGAAAATCGA TGTTTTCGCT TTTGGGGTGG
5. 7.1306 7.45	11 AAAAA 1 (
Frisson	TTCTGATTGA GTTGCTTACC GGCAAGAAAG CGATAACAAC GATGGAAAAT
Finale	TTCTGATTGA GTTGCTTACC CXCAAGAAAG CGATAACAAC GATGGAAAAT
Frisson	GGCGAGGTGG TTATTCTGTG GAAGGATTTC TGGAAGATTT TTGATCTAGA
Finale	GGCCAGGTGG TTATTCTGTG GAAGGATTTC TGGAAGATTT TTGATCTAGA
÷	3.77.53.77.48. 01.4.52.02.02.00.00.00.00.00.00.00.00.00.00.00
Frisson Finale	AGGGAATAGA GAAGAGAGCT TAAGAAAATG GATGGATCCT AAGCTAGAGA
truars	AGGGAATAGA GAAGAGAGCT TAAGAAAATG GATGGATCCT AAGCTAGAGA

grisson	ATTTTTATCC TATTGATAAT OCTCTTAGTT TGGCTTCTTT GGCAGTGAAT
Finale	ATTITITATIC TATTGATAAT GCTCTTAGTT TXGCTTCTTT GGCAGTXAAT
0.0040000000	
Frieson	TGUACTGCAG ATAAATCATT GTCAAGACCA AGCATTGCAG AAATTGTTCT
Finale	TOTACTOCAG ATAAATCATT GTCAAGACCA AGCATTGCAG AAATTGTTCT
to define the rest on .	
Prisson	TIGICITICI CITCICAATO AATCATCATO TOAACCAATO TIAGAAAGAT
Finale	TYGTOTTTCT CTTCTCAATC AATCATCATC TGAACCAATG TTAGAAAGAT
Prisson	COTTGACATO TOGTYTAGAT GTTGAAGCTA CYCATUTYGT TACTYCTATA
Finale	CONTRACATO TRESTAGAT RITRAARCIA CICATUITUT TACITOTATA
Frisson	GTAGCTCGTT GATATTCATT CAAGTGAAGG TAACACT
Finale	GTAGCTCGTT GATATTCATT CAAGTGANGG TAACACTNAA TCAATGCTTC
Prisson	AGETYCTTAT ATTCAACATC GTTACTITGT TIAG <mark>A</mark> TGATI ATTGATTACA
Finale	AGTITUTTAT ATTUAAGATO OTTACTTTUT TTAGETGATT ATTUATTACA
Prisson	TOTTTATOTO TOGAACTATA TOOTTATTIT AATTAACKKA ATT
Finale	TOTTIATOTO TOGRACIATA TEXTIATITE AATTAACEEA ATT
Frisson	ANTICATITY TOCATOTT SEC ID NO: 13
Finale	arthartet tocatott <u>SEQ ID MO. 12</u>

^{*} Nucleotide differences are shaded black and the coding region is underlined